EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
S1	1	("6255458").PN.	USPAT; USOCR	OR	OFF	2006/12/21 16:36
S2	1	("5326696").PN.	USPAT; USOCR	OR	OFF	2006/12/19 18:52
S3	2439	immunoglobulin heavy chain	USPAT	ADJ	ON	2006/12/20 18:36
S4	1501	S3 and constant region	USPAT	ADJ	ON	2006/12/20 18:36
S5	19	S4 and real-time pcr	USPAT	ADJ	ON	2006/12/20 18:39
S6	0	constant region real-time pcr	USPAT	SAME	ON	2006/12/20 18:40
S7	2	heavy chain real-time pcr	USPAT	SAME	ON	2006/12/20 18:40
S8	1	("5919910").PN.	USPAT; USOCR	OR	OFF	2006/12/21 10:59
S9	1	("6096878").PN.	USPAT; USOCR	OR	OFF	2006/12/21 11:33
S10	1	("6096878").PN.	USPAT; USOCR	OR	OFF	2006/12/21 12:24
S11	1	("6096878").PN.	USPAT; USOCR	OR	OFF	2006/12/21 15:05
S12	3875	constant region immunoglobulin	USPAT	WITH	ON	2006/12/21 15:06
S13	2424	constant region immunoglobulin	USPAT	NEAR	ON	2006/12/21 15:06
S14	92	constant region sequence immunoglobulin	USPAT	NEAR	ON	2006/12/21 15:06
S15	1	("6652852").PN.	USPAT; USOCR	OR	OFF	2006/12/21 16:37

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 97.9733 Seconds
                                              (without alignments)
                                              358.960 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA_New:*
                 1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	48	7	US-11-241-154-39	Sequence 39, Appl
2	22	100.0	291	7	US-11-241-154-49	Sequence 49, Appl
3	22	100.0	310	6	US-10-534-800-52	Sequence 52, Appl
4	22	100.0	312	6	US-10-534-800-51	Sequence 51, Appl
5	22	100.0	336	7	US-11-241-154-9	Sequence 9, Appli
6	22	100.0	351	9	US-11-171-085-1	Sequence 1, Appli
7	22	100.0	367	8	US-11-266-748A-59272	Sequence 59272, A

rnpbm — 11

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 844.8 Seconds
                                             (without alignments)
                                             319.991 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries.

Database :   Published_Applications_NA_Main:*
          1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
          2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
          3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
          4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
          5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
          6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
          7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
          8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
          9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
         10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
         11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
         12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
         13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
         14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
         15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
         16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   22   100.0   48 7   US-10-338-366-39   Sequence 39, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 77.1467 Seconds
                                             (without alignments)
                                             533.586 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	22	100.0	48	2	US-08-477-553A-16	Sequence 16, Appl
2	22	100.0	48	2	US-08-477-553A-17	Sequence 17, Appl
3	22	100.0	243	3	US-09-042-353-148	Sequence 148, App
4	22	100.0	243	3	US-08-758-417A-412	Sequence 412, App
5	22	100.0	282	3	US-09-042-353-149	Sequence 149, App
6	22	100.0	282	3	US-08-758-417A-413	Sequence 413, App
7	22	100.0	285	3	US-09-042-353-150	Sequence 150, App

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 2128.13 Seconds
                                             (without alignments)
                                             578.077 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_gss1:*
                 12: gb_gss2:*
                 13: gb_gss3:*
                 14: gb_gss4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
  No.   Score Match Length DB ID   Description
----
      1   22 100.0   125 3 BQ376743   BQ376743 CM3-UM003
      2   22 100.0   125 7 BE155965   BE155965 QV0-HT036
      3   22 100.0   161 2 BF771951   BF771951 RC6-IT002

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 1143.12 Seconds
                                             (without alignments)
                                             1230.705 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % | | | | |
| Result | | Query | | | | |
No.	Score	Match	Length	DB	ID	Description
1	22	100.0	22	2	CS112296	CS112296 Sequence
2	22	100.0	22	2	CS122886	CS122886 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 254.027 Seconds
                                          (without alignments)
                                          603.832 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_8:*
              1: geneseqn1980s:*
              2: geneseqn1990s:*
              3: geneseqn2000s:*
              4: geneseqn2001as:*
              5: geneseqn2001bs:*
              6: geneseqn2002as:*
              7: geneseqn2002bs:*
              8: geneseqn2003as:*
              9: geneseqn2003bs:*
              10: geneseqn2003cs:*
              11: geneseqn2003ds:*
              12: geneseqn2004as:*
              13: geneseqn2004bs:*
              14: geneseqn2005s:*
              15: geneseqn2006s:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   22 100.0   22 14   AEA61513   Aea61513 VH4 forwa
     2   22 100.0   22 14   AEB16529   Aeb16529 Human Ig

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 80.16 Seconds
                                             (without alignments)
                                  358.960 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagcccgggggag 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA_New:*
      1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
      2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
      3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
      4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
      5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
      6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
      7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
      8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
      9:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
      10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	90	9	US-11-365-556-251	Sequence 251, App
2	18	100.0	90	9	US-11-365-556-252	Sequence 252, App
3	18	100.0	363	8	US-11-337-300-362	Sequence 362, App
4	18	100.0	369	6	US-10-499-266-11	Sequence 11, Appl
5	18	100.0	742	6	US-10-539-402-47	Sequence 47, Appl
6	18	100.0	765	8	US-11-337-300-241	Sequence 241, App
7	18	100.0	1237661	8	US-11-266-748A-29041	Sequence 29041, A

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 691.2 Seconds
                                             (without alignments)
                                             319.991 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagcccgggggag 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA_Main:*
         1:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
         2:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
         3:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
         4:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
         5:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
         6:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
         7:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
         8:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
         9:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
        10:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
        11:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
        12:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
        13:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
        14:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
        15:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
        16:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                          %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
  c   1   18 100.0   45 10   US-10-920-899-1061   Sequence 1061, Ap

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 63.12 Seconds
                                             (without alignments)
                                             533.586 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagcccggggag 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	369	3	US-09-513-999C-42	Sequence 42, Appl
2	18	100.0	372	3	US-09-513-999C-43	Sequence 43, Appl
3	18	100.0	414	3	US-09-042-353-353	Sequence 353, App
4	18	100.0	414	3	US-08-758-417A-201	Sequence 201, App
5	18	100.0	421	3	US-09-905-243-6	Sequence 6, Appli
6	18	100.0	427	3	US-09-905-243-3	Sequence 3, Appli
7	18	100.0	429	3	US-09-513-999C-40	Sequence 40, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 1741.2 Seconds
                                            (without alignments)
                                            578.077 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagcccgggggag 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_gss1:*
                 12: gb_gss2:*
                 13: gb_gss3:*
                 14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB ID   Description
----
       1   18 100.0   275 7 AW403407   AW403407 UI-HF-BK0
       2   18 100.0   283 7 BE241696   BE241696 TCAAP1E04
       3   18 100.0   310 7 AW403418   AW403418 UI-HF-BK0

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 935.28 Seconds
                                           (without alignments)
                                           1230.705 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagcccgggggag 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 ,. Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                1: gb_env:*
                2: gb_pat:*
                3: gb_ph:*
                4: gb_pl:*
                5: gb_pr:*
                6: gb_ro:*
                7: gb_sts:*
                8: gb_sy:*
                9: gb_un:*
                10: gb_vi:*
                11: gb_ov:*
                12: gb_htg:*
                13: gb_in:*
                14: gb_om:*
                15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
      1   18 100.0   18 2   CS112298   CS112298 Sequence
      2   18 100.0   18 2   CS122888   CS122888 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 207.84 Seconds
                                             (without alignments)
                                             603.832 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagcccgggggag 18

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: ·   5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 ·

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_8:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002as:*
                  7: geneseqn2002bs:*
                  8: geneseqn2003as:*
                  9: geneseqn2003bs:*
                  10: geneseqn2003cs:*
                  11: geneseqn2003ds:*
                  12: geneseqn2004as:*
                  13: geneseqn2004bs:*
                  14: geneseqn2005s:*
                  15: geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score Match Length DB ID   Description
----
      1   18   100.0   18   14 AEA61515   Aea61515 VH5 forwa
      2   18   100.0   18   14 AEB16531   Aeb16531 Human Ig

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 75.7067 Seconds
                                            (without alignments)
                                 358.960 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17	100.0	864	8	US-11-154-103-29	Sequence 29, Appl
c 2	17	100.0	1633	8	US-11-266-748A-357372	Sequence 357372,
3	17	100.0	1633	8	US-11-266-748A-440751	Sequence 440751,
4	17	100.0	2428	1	US-09-798-279D-1	Sequence 1, Appli
c 5	17	100.0	1237661	8	US-11-266-748A-29041	Sequence 29041, A
c 6	16	94.1	77	8	US-11-255-820-10	Sequence 10, Appl
7	16	94.1	1865	8	US-11-266-748A-258582	Sequence 258582,

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 652.8 Seconds
                                              (without alignments)
                                              319.991 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA_Main:*
            1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
            2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
            3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
            4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
            5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
            6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
            7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
            8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
            9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
           10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
           11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
           12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
           13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
           14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
           15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
           16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
 c   1   17   100.0   52 10   US-10-941-768A-1   Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 59.6133 Seconds
                                            (without alignments)
                                            533.586 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggcccccagtgctg 17

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17	100.0	52	3	US-09-724-138-1	Sequence 1, Appli
c 2	17	100.0	52	3	US-09-630-198-1	Sequence 1, Appli
c 3	17	100.0	69	2	US-08-053-131-129	Sequence 129, App
c 4	17	100.0	69	2	US-08-645-641-129	Sequence 129, App
c 5	17	100.0	69	2	US-07-853-408B-129	Sequence 129, App
c 6	17	100.0	69	2	US-08-096-762-129	Sequence 129, App
c 7	17	100.0	69	2	US-08-308-865-129	Sequence 129, App

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 1644.47 Seconds
                                          (without alignments)
                                          578.077 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggcccagtgctg 17

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_gss1:*
                12: gb_gss2:*
                13: gb_gss3:*
                14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	100.0	233	2	BG986365	BG986365 CM1-HT114
2	17	100.0	246	7	BB032646	BB032646 BB032646
3	17	100.0	324	11	AQ077340	AQ077340 CIT-HSP-2

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 883.32 Seconds
                                              (without alignments)
                                              1230.705 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                1: gb_env:*
                2: gb_pat:*
                3: gb_ph:*
                4: gb_pl:*
                5: gb_pr:*
                6: gb_ro:*
                7: gb_sts:*
                8: gb_sy:*
                9: gb_un:*
                10: gb_vi:*
                11: gb_ov:*
                12: gb_htg:*
                13: gb_in:*
                14: gb_om:*
                15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   17   100.0   17   2 CS112301   CS112301 Sequence
     2   17   100.0   17   2 CS122891   CS122891 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 196.293 Seconds
                                              (without alignments)
                                              603.832 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_8:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result   Query
  No.   Score   Match Length DB ID   Description
----
     1   17 100.0   17 14 AEA61518   Aea61518 JH1 forwa
     2   17 100.0   17 14 AEB16534   Aeb16534 Human Ig

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 80.16 Seconds
                                             (without alignments)
                                           358.960 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA_New:*
           1:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
           2:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
           3:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
           4:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
           5:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
           6:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
           7:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
           8:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
           9:    /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
           10:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result   %
                 Query
     No.   Score Match Length DB ID   Description
        ----
     c   1   18 100.0   348 7 US-11-241-154-5   Sequence 5, Appli
     c   2   18 100.0   354 7 US-11-145-131A-1   Sequence 1, Appli
     c   3   18 100.0   354 7 US-11-145-131A-5   Sequence 5, Appli
     c   4   18 100.0   377 8 US-11-266-748A-61653   Sequence 61653, A
     c   5   18 100.0   411 8 US-11-291-668-54   Sequence 54, Appl
     c   6   18 100.0   411 8 US-11-292-164-54   Sequence 54, Appl
     c   7   18 100.0   583 8 US-11-266-748A-176280   Sequence 176280,

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.OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 691.2 Seconds
                                             (without alignments)
                                           319.991 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA_Main:*
            1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
            2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
            3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
            4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
            5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
            6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
            7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
            8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
            9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
           10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
           11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
           12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
           13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
           14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
           15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
           16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
  c   1   18   100.0   32   16   US-11-009-840A-334   Sequence 334, App

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 63.12 Seconds
                                             (without alignments)
                                             533.586 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

               %
Result   Query
   No. Score Match Length DB   ID   Description
----
c 1   18   100.0   32   3   US-09-042-353-70   Sequence 70, Appl
c 2   18   100.0   32   3   US-08-758-417A-334   Sequence 334, App
c 3   18   100.0   39   3   US-09-042-353-86   Sequence 86, Appl
c 4   18   100.0   39   3   US-08-758-417A-350   Sequence 350, App
c 5   18   100.0   53   3   US-09-724-138-2   Sequence 2, Appli
c 6   18   100.0   53   3   US-09-630-198-2   Sequence 2, Appli
c 7   18   100.0   94   2   US-08-053-131-141   Sequence 141, App

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 1741.2 Seconds
                                             (without alignments)
                                             578.077 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_gss1:*
                12: gb_gss2:*
                13: gb_gss3:*
                14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description
   ----
   c   1   18 100.0   126 1   AA866589   AA866589 CJC116 HT
   c   2   18 100.0   266 1   AA402547   AA402547 zu47h07.r
   c   3   18 100.0   318 10   F08009   F08009 HSC2NH041 n

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 935.28 Seconds
                                             (without alignments)
                                             1230.705 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

         %
Result   Query
  No.   Score Match Length DB ID   Description
----
      1   18 100.0   18 2 CS112302   CS112302 Sequence
      2   18 100.0   18 2 CS122892   CS122892 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 207.84 Seconds
                                         (without alignments)
                                         603.832 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq.length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_8:*
               1: geneseqn1980s:*
               2: geneseqn1990s:*
               3: geneseqn2000s:*
               4: geneseqn2001as:*
               5: geneseqn2001bs:*
               6: geneseqn2002as:*
               7: geneseqn2002bs:*
               8: geneseqn2003as:*
               9: geneseqn2003bs:*
               10: geneseqn2003cs:*
               11: geneseqn2003ds:*
               12: geneseqn2004as:*
               13: geneseqn2004bs:*
               14: geneseqn2005s:*
               15: geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No. Score Match Length DB ID   Description
----
      1   18 100.0   18 14 AEA61519   Aea61519 JH2 forwa
      2   18 100.0   18 14 AEB16535   Aeb16535 Human Ig

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:46:28 ; Search time 85.0571 Seconds
                                             (without alignments)
                                             313.422 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2931743 seqs, 1025338116 residues

Total number of hits satisfying chosen parameters: 5863486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
                11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	73	10	US-11-388-794-4	Sequence 4, Appli
c 2	13	100.0	426	6	US-10-374-780A-1368	Sequence 1368, Ap
3	13	100.0	495	10	US-11-388-794-1	Sequence 1, Appli
c 4	13	100.0	580	8	US-11-266-748A-19187	Sequence 19187, A
5	13	100.0	639	6	US-10-953-349-13124	Sequence 13124, A
6	13	100.0	641	6	US-10-953-349-18139	Sequence 18139, A

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:43:44 ; Search time 489.914 Seconds
                                              (without alignments)
                                              326.056 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description
----
 c   1   13 100.0   213   7 US-10-156-761-7473   Sequence 7473, Ap

rni-34

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:38:28 ; Search time 58.6857 Seconds
                                              (without alignments)
                                              414.486 Million cell updates/sec

Title: US-10-734-622-34
Perfect score:.   13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                  1:   /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                  2:   /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                  3:   /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                  4:   /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                  5:   /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                  6:   /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                  7:   /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                  8:   /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                  9:   /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                  10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
    No.   Score   Match Length DB   ID   Description
     ----
       1   13   100.0   270   3 US-09-902-540-3340   Sequence 3340, Ap
       2   13   100.0   372   3 US-09-902-540-7383   Sequence 7383, Ap
       3   13   100.0   396   2 US-08-470-179-34   Sequence 34, Appl
   c   4   13   100.0   663   3 US-09-902-540-9035   Sequence 9035, Ap
       5   13   100.0   711   3 US-09-902-540-6527   Sequence 6527, Ap
       6   13   100.0   726   3 US-09-902-540-3401   Sequence 3401, Ap
   c   7   13   100.0   873   3 US-09-902-540-5251   Sequence 5251, Ap

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:31:30 ; Search time 1661.03 Seconds
                                              (without alignments)
                                              437.651 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_gss1:*
                12: gb_gss2:*
                13: gb_gss3:*
                14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES

              %
Result   Query
   No.   Score Match Length DB ID   Description
----
    1   13 100.0   123 8   CN146538   CN146538 WOUND1_41
c   2   13 100.0   136 13 CL818456   CL818456 OR_CBa003
    3   13 100.0   140 10 DW401021   DW401021 LRAGE0058

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:23:30 ; Search time 801.914 Seconds
                                              (without alignments)
                                              1036.665 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   13   100.0   13   2   CS112319   CS112319 Sequence
c   2   13   100.0   73   2   CS059461   CS059461 Sequence

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:19:50 ; Search time 174.2 Seconds
                                              (without alignments)
                                              520.317 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_8:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   13   100.0   13 14   AEA61536   Aea61536 IgG CH pr
  c 2   13   100.0   73 14   ADZ00236   Adz00236 Melanoma

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:46:28 ; Search time 143.943 Seconds
                                          (without alignments)
                                        313.422 Million cell updates/sec

Title: US-10-734-622-35
Perfect score: 22
Sequence: 1 aagtagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 2931743 seqs, 1025338116 residues

Total number of hits satisfying chosen parameters: 5863486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
           1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
           2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
           3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
           4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
           5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
           6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
           7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
           8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
           9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
          10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
          11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	22	100.0	294	8	US-11-219-563-137	Sequence 137, App
c 2	22	100.0	447	1	US-09-784-950-74	Sequence 74, Appl
c 3	22	100.0	477	1	US-09-784-950-78	Sequence 78, Appl
c 4	22	100.0	503	1	US-09-784-950-79	Sequence 79, Appl
c 5	22	100.0	519	1	US-09-784-950-76	Sequence 76, Appl
c 6	22	100.0	524	10	US-11-349-724-219	Sequence 219, App

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:43:44 ; Search time 829.086 Seconds
                                              (without alignments)
                                      326.056 Million cell updates/sec

Title: US-10-734-622-35
Perfect score: 22
Sequence: 1 aagtagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
         1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
         2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
         3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
         4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
         5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
         6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
         7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
         8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
         9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
        10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
        11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
        12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
        13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
        14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
        15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
        16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
 c   1   22   100.0   64   7   US-10-199-957A-115.   Sequence 115, App

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:38:28 ; Search time 99.3143 Seconds
                                              (without alignments)
                                              414.486 Million cell updates/sec

Title: US-10-734-622-35
Perfect score: 22
Sequence: 1 aagtagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
               1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
               2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
               3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
               4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
               5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
               6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
               7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
               8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
               9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
               10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	29	2	US-07-905-040-13	Sequence 13, Appl
2	22	100.0	29	2	US-08-021-619-13	Sequence 13, Appl
3	22	100.0	29	7	PCT-US93-01880-13	Sequence 13, Appl
c 4	22	100.0	30	2	US-08-263-258-6	Sequence 6, Appli
c 5	22	100.0	30	7	PCT-US93-12501-10	Sequence 10, Appl
c 6	22	100.0	329	3	US-09-023-655-1383	Sequence 1383, Ap
c 7	22	100.0	348	3	US-09-171-945-23	Sequence 23, Appl

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:31:30 ; Search time 2810.97 Seconds

(without alignments)

437.651 Million cell updates/sec

Title: US-10-734-622-35

Perfect score: 22

Sequence: 1 aagtagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :   EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

7: gb_est2:*

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:23:30 ; Search time 1357.09 Seconds
                                                (without alignments)
                                                1036.665 Million cell updates/sec

Title: US-10-734-622-35
Perfect score: 22
Sequence: 1 aagtagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_env:*
                2: gb_pat:*
                3: gb_ph:*
                4: gb_pl:*
                5: gb_pr:*
                6: gb_ro:*
                7: gb_sts:*
                8: gb_sy:*
                9: gb_un:*
               10: gb_vi:*
               11: gb_ov:*
               12: gb_htg:*
               13: gb_in:*
               14: gb_om:*
               15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                     %
Result   Query
  No.   Score Match Length DB   ID   Description
----
     1   22 100.0   22   2 CS112320   CS112320 Sequence
     2   22 100.0   22   2 CS122910   CS122910 Sequence

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:19:50 ; Search time 294.8 Seconds
                                          (without alignments)
                                 520.317 Million cell updates/sec

Title: US-10-734-622-35
Perfect score: 22
Sequence: 1 aagtagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_8:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*
                14: geneseqn2005s:*
                15: geneseqn2006s:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
      1   22 100.0   22   14   AEA61537   Aea61537 IgG CH pr
      2   22 100.0   22   14   AEB16553   Aeb16553 Human IgG